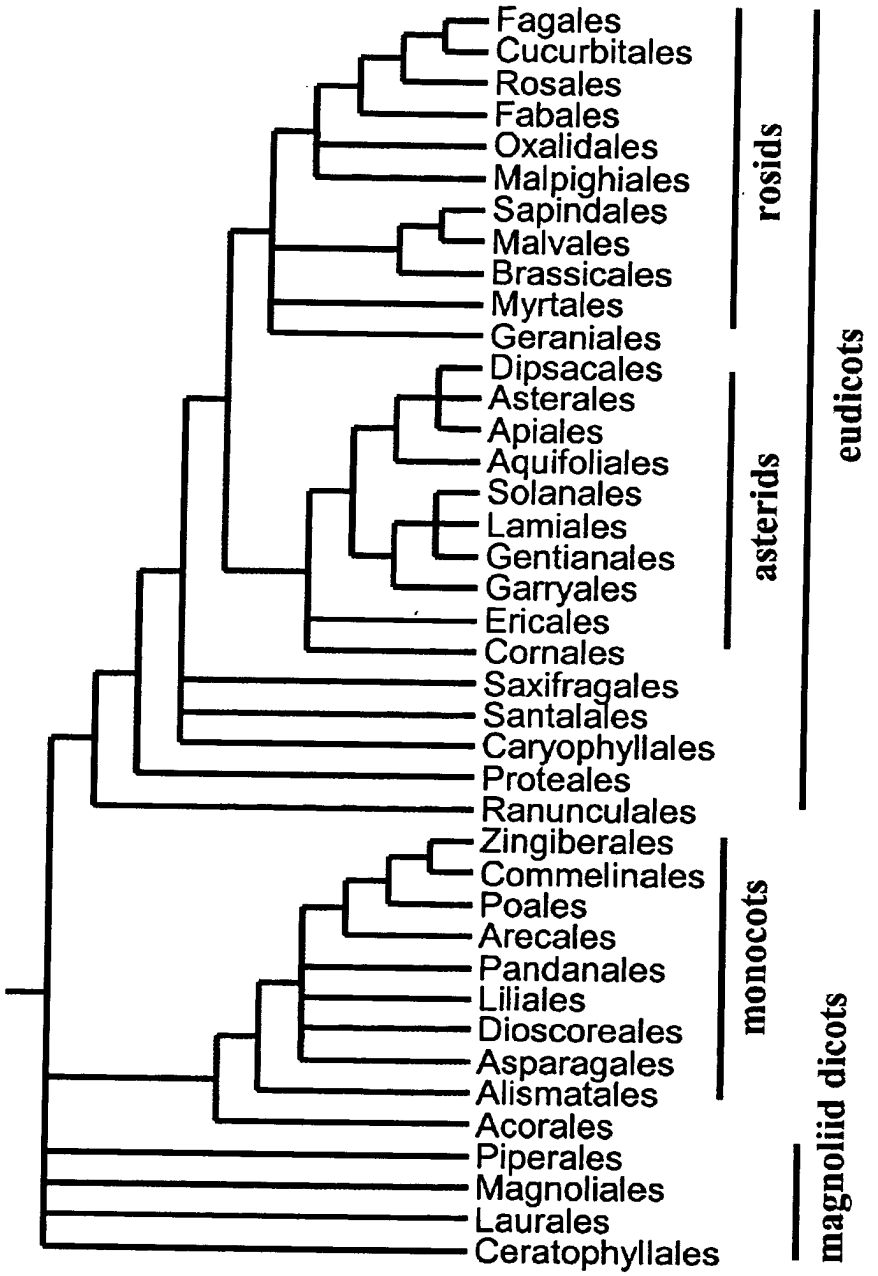

Fagales
Cucurbitales
Rosales
Fabales
Oxalidales
Malpighiales
Sapindales
Malvales
Brassicales
Myrtales
Geraniales
Dipsacales
Asterales
Apiales
Aquifoliales
Solanales
Lamiales
Gentianales
Garryales
Ericales
Cornales
Saxifragales
Santalales
Caryophyllales
Proteales
Ranunculales
Zingiberales
Commelinales
Poales
Arecales
Pandanales
Liliales
Dioscoreales
Asparagales
Alismatales
Acorales
Piperales
Magnoliales
Laurales
Ceratophyllales
rosids
asterids
eudicots
monocots
magnoliid dicots

FIGURE 1

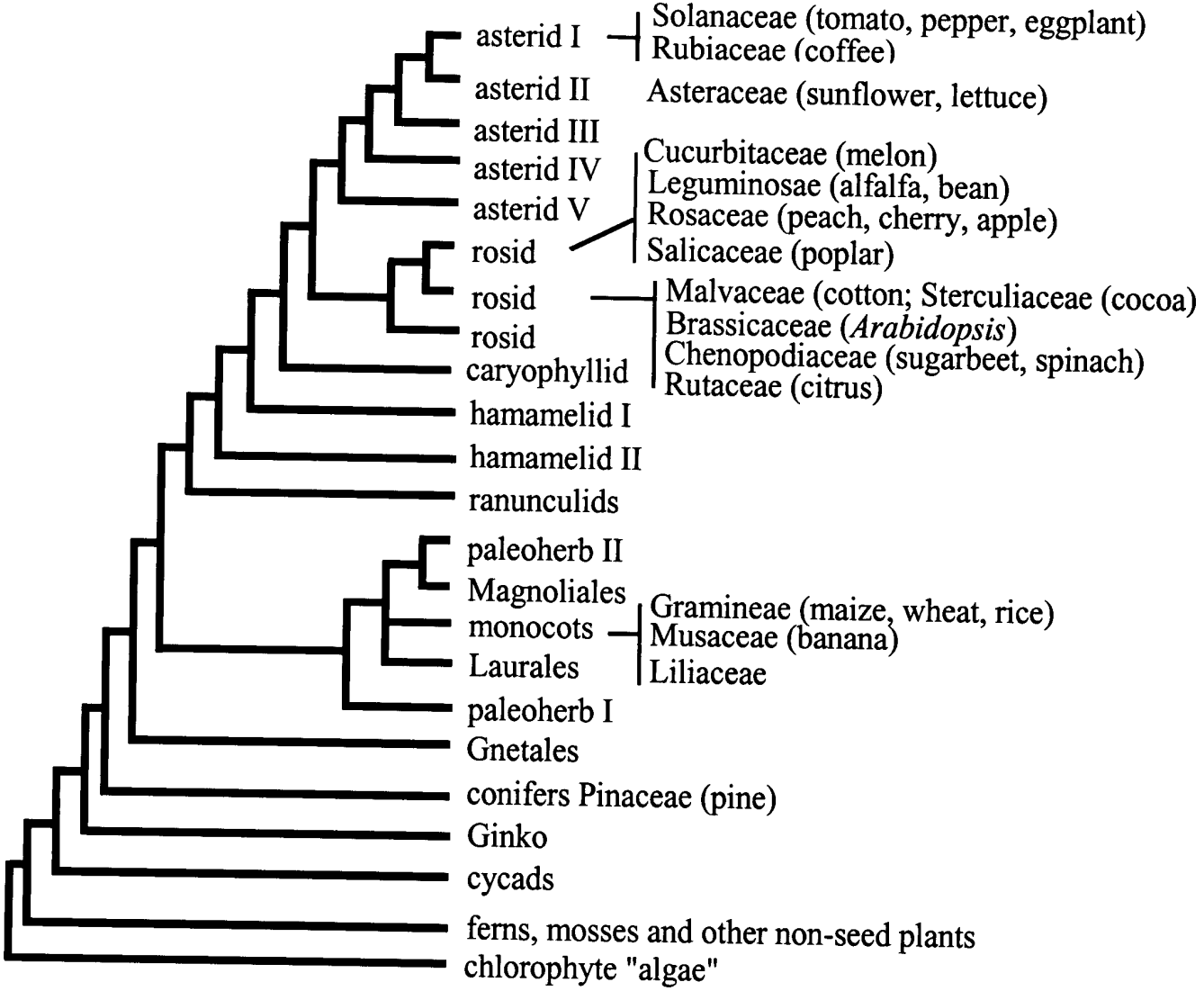

asterid I
asterid II
asterid III
asterid IV
asterid V
rosid
rosid
rosid
caryophyllid
hamamelid I
hamamelid II
ranunculids
paleoherb II
Magnoliales
monocots
Laurales
paleoherb I
Gnetales
conifers Pinaceae (pine)
Ginko
cycads
ferns, mosses and other non-seed plants
chlorophyte "algae"
Solanaceae (tomato, pepper, eggplant)
Rubiaceae (coffee)
Asteraceae (sunflower, lettuce)
Cucurbitaceae (melon)
Leguminosae (alfalfa, bean)
Rosaceae (peach, cherry, apple)
Salicaceae (poplar)
Malvaceae (cotton; Sterculiaceae (cocoa)
Brassicaceae (*Arabidopsis*)
Chenopodiaceae (sugarbeet, spinach)
Rutaceae (citrus)
Gramineae (maize, wheat, rice)
Musaceae (banana)
Liliaceae

FIGURE 2

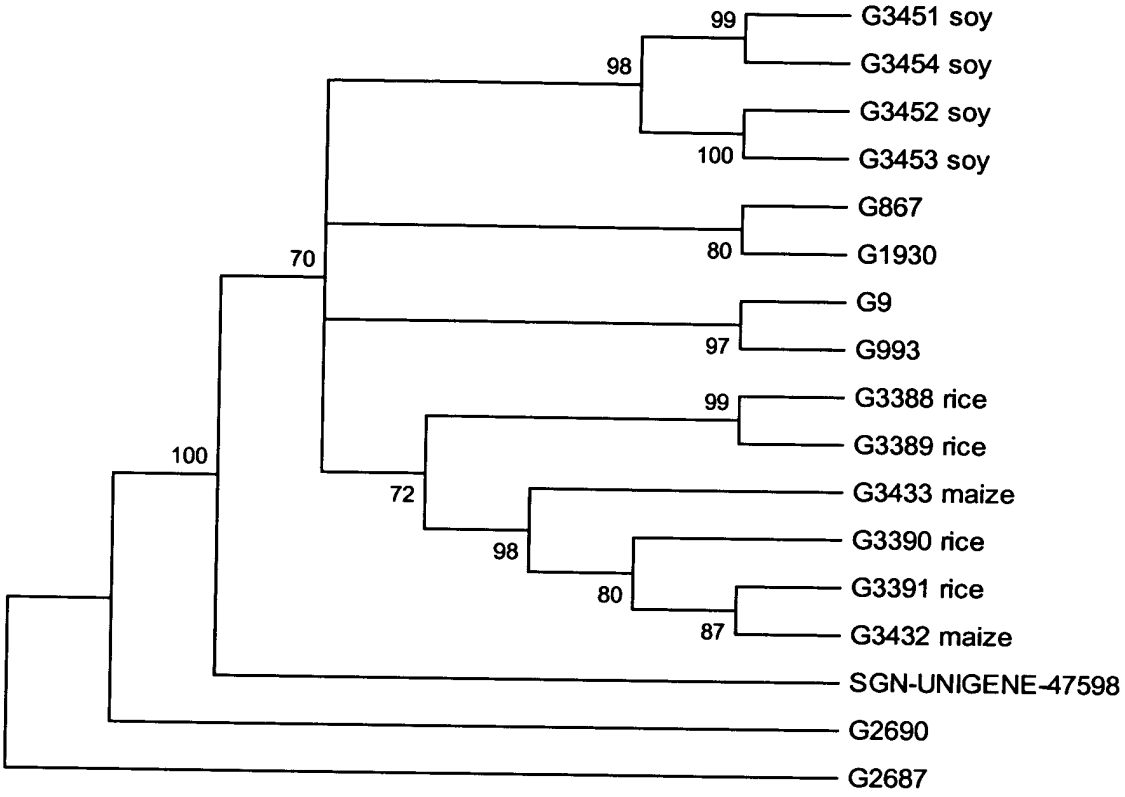
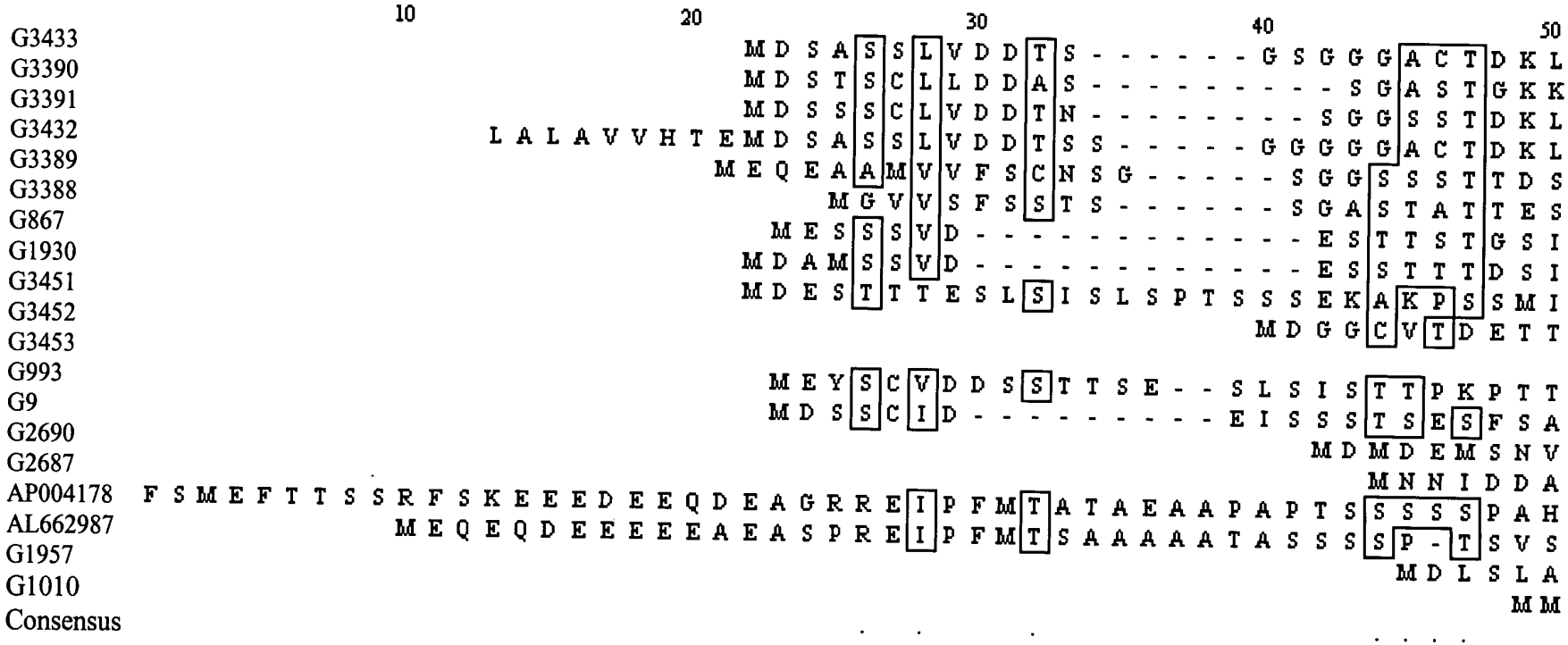

99
G3451 soy
98
G3454 soy
G3452 soy
100
G3453 soy
G867
80
G1930
70
G9
97
G993
99
G3388 rice
G3389 rice
100
72
G3433 maize
G3390 rice
98
80
G3391 rice
87
G3432 maize
SGN-UNIGENE-47598
G2690
G2687

FIGURE 3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20
30
40
50
G3433
G3390
G3391
G3432
G3389
G3388
G867
G1930
G3451
G3452
G3453
G993
G9
G2690
G2687
AP004178
AL662987
G1957
G1010
Consensus

FIGURE 4A

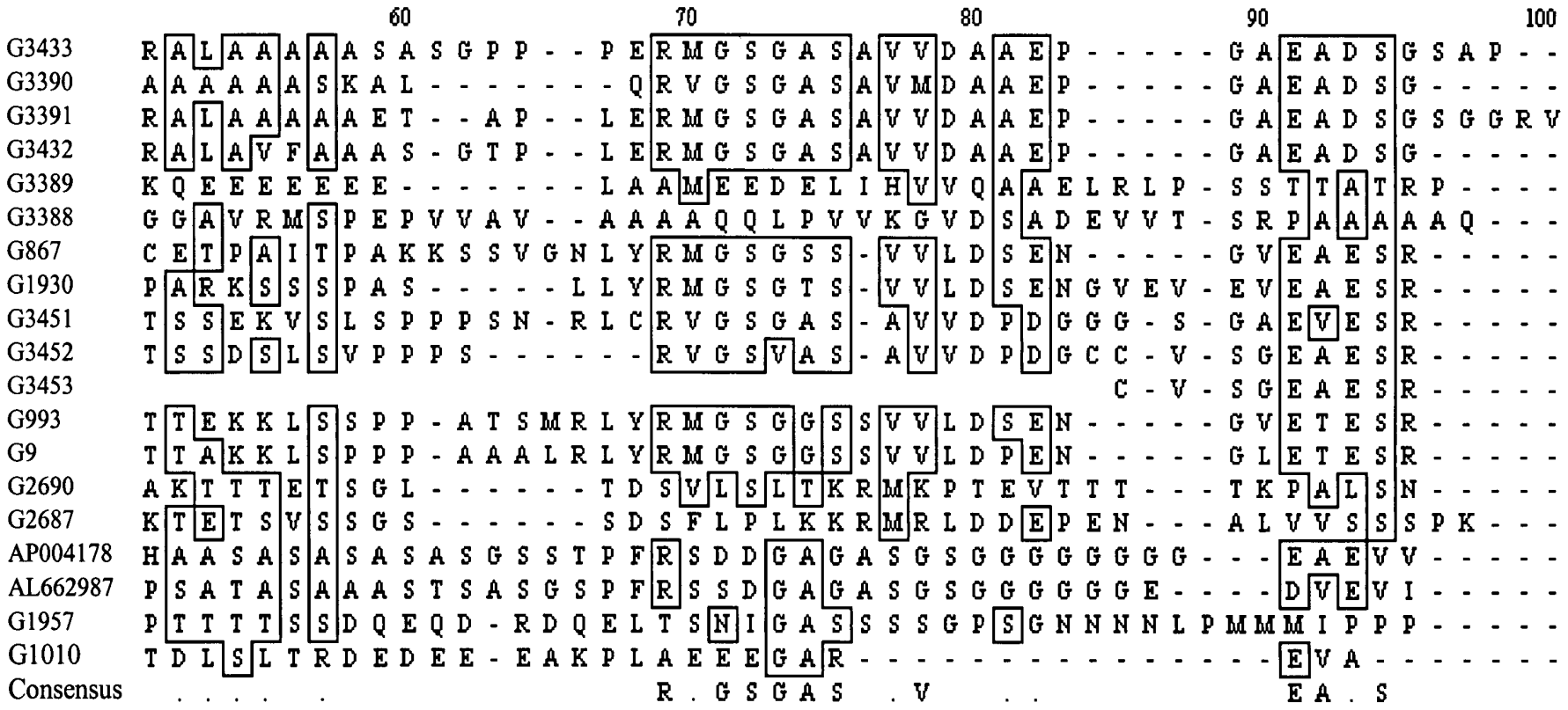

60
70
80
90
100
G3433
G3390
G3391
G3432
G3389
G3388
G867
G1930
G3451
G3452
G3453
G993
G9
G2690
G2687
AP004178
AL662987
G1957
G1010
Consensus

FIGURE 4B

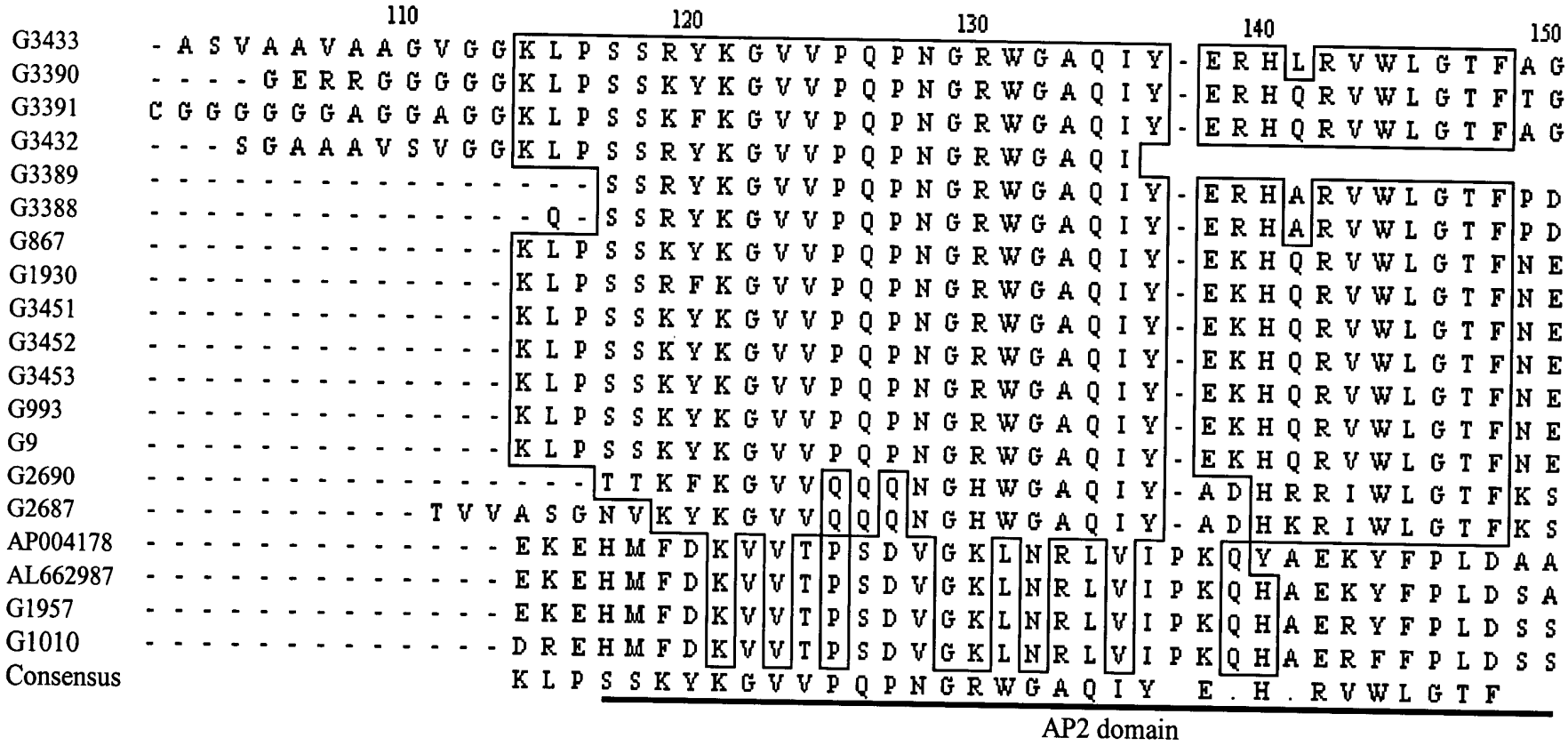

110
120
130
140
150
G3433 - A S V A A V A A G V G G K L P S S R Y K G V V P Q P N G R W G A Q I Y - E R H L R V W L G T F A G
G3390 - - - - G E R R G G G G G K L P S S K Y K G V V P Q P N G R W G A Q I Y - E R H Q R V W L G T F T G
G3391 C G G G G G G A G G A G G K L P S S K F K G V V P Q P N G R W G A Q I Y - E R H Q R V W L G T F A G
G3432 - - - S G A A A V S V G G K L P S S R Y K G V V P Q P N G R W G A Q I
G3389 - - - - - - - - - - - - - - - - S S R Y K G V V P Q P N G R W G A Q I Y - E R H A R V W L G T F P D
G3388 - - - - - - - - - - - - - - Q - S S R Y K G V V P Q P N G R W G A Q I Y - E R H A R V W L G T F P D
G867 - - - - - - - - - - - - - K L P S S K Y K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G1930 - - - - - - - - - - - - - K L P S S R F K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G3451 - - - - - - - - - - - - - K L P S S K Y K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G3452 - - - - - - - - - - - - - K L P S S K Y K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G3453 - - - - - - - - - - - - - K L P S S K Y K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G993 - - - - - - - - - - - - - K L P S S K Y K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G9 - - - - - - - - - - - - - K L P S S K Y K G V V P Q P N G R W G A Q I Y - E K H Q R V W L G T F N E
G2690 - - - - - - - - - - - - - - - - T T K F K G V V Q Q Q N G H W G A Q I Y - A D H R R I W L G T F K S
G2687 - - - - - - - - - - T V V A S G N V K Y K G V V Q Q Q N G H W G A Q I Y - A D H K R I W L G T F K S
AP004178 - - - - - - - - - - - - - E K E H M F D K V V T P S D V G K L N R L V I P K Q Y A E K Y F P L D A A
AL662987 - - - - - - - - - - - - - E K E H M F D K V V T P S D V G K L N R L V I P K Q H A E K Y F P L D S A
G1957 - - - - - - - - - - - - - E K E H M F D K V V T P S D V G K L N R L V I P K Q H A E R Y F P L D S S
G1010 - - - - - - - - - - - - - D R E H M F D K V V T P S D V G K L N R L V I P K Q H A E R F F P L D S S
Consensus K L P S S K Y K G V V P Q P N G R W G A Q I Y E . H . R V W L G T F
AP2 domain

FIGURE 4C

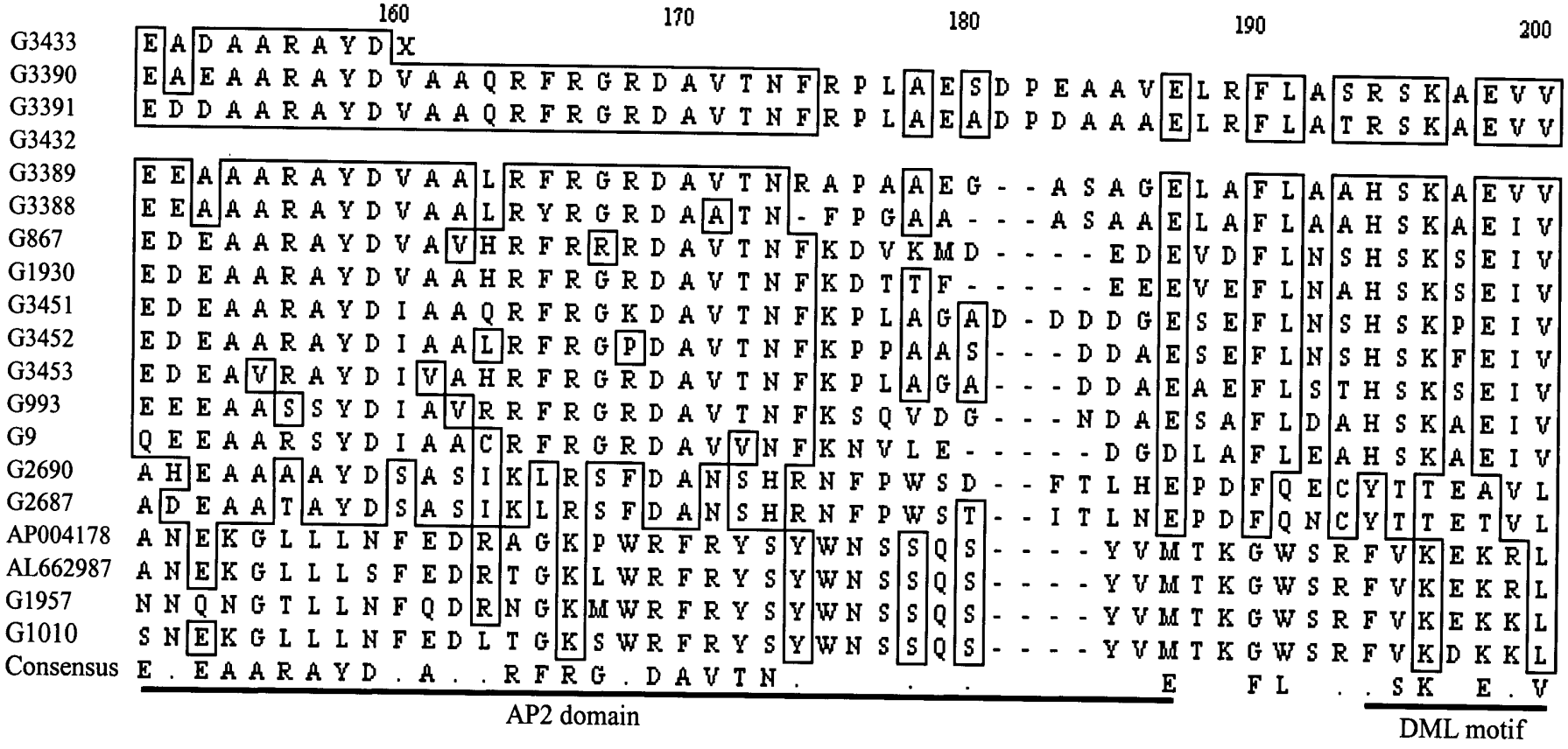

160
170
180
190
200
G3433
G3390
G3391
G3432
G3389
G3388
G867
G1930
G3451
G3452
G3453
G993
G9
G2690
G2687
AP004178
AL662987
G1957
G1010
Consensus
AP2 domain
DML motif

FIGURE 4D

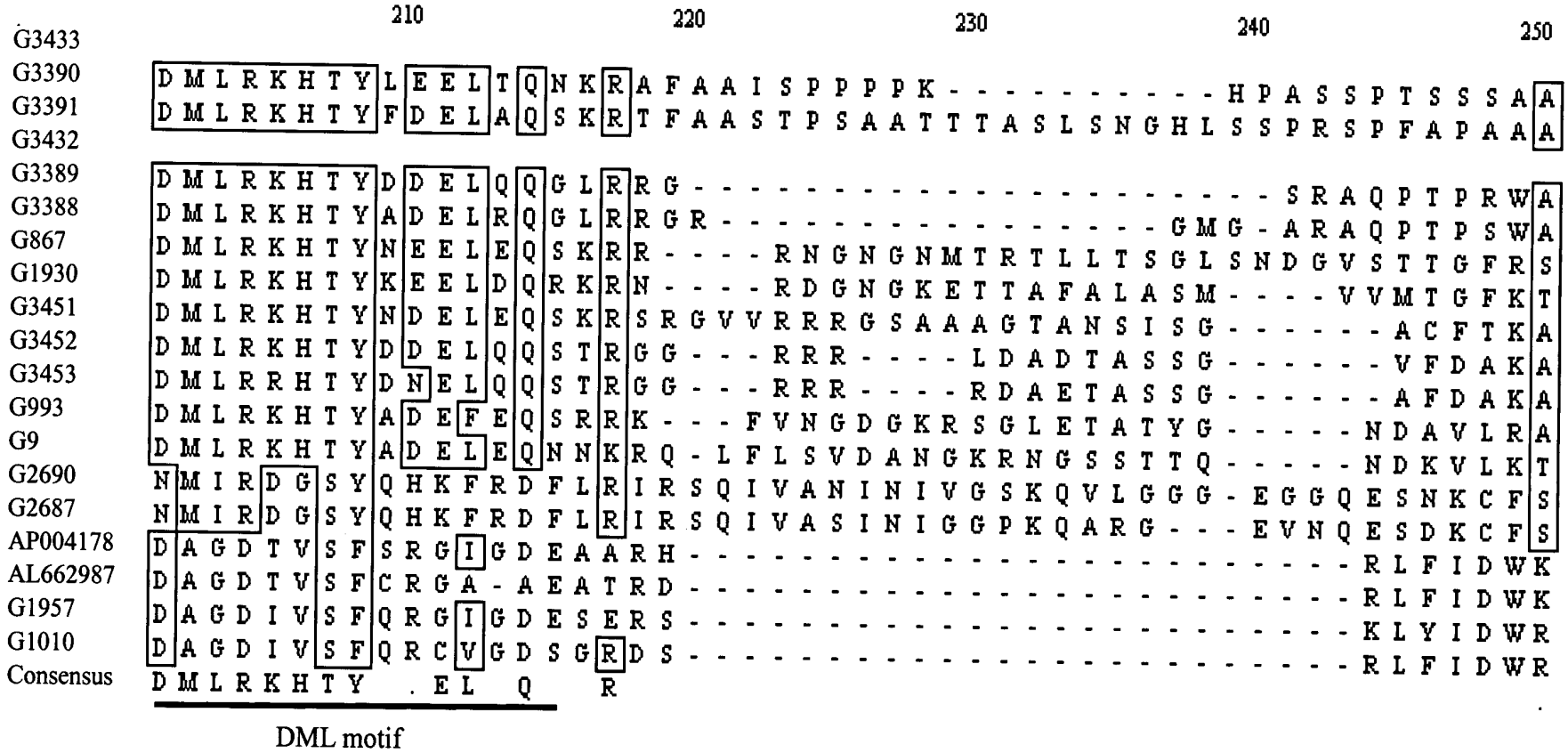

210
220
230
240
250
G3433
G3390
G3391
G3432
G3389
G3388
G867
G1930
G3451
G3452
G3453
G993
G9
G2690
G2687
AP004178
AL662987
G1957
G1010
Consensus
DML motif

FIGURE 4E

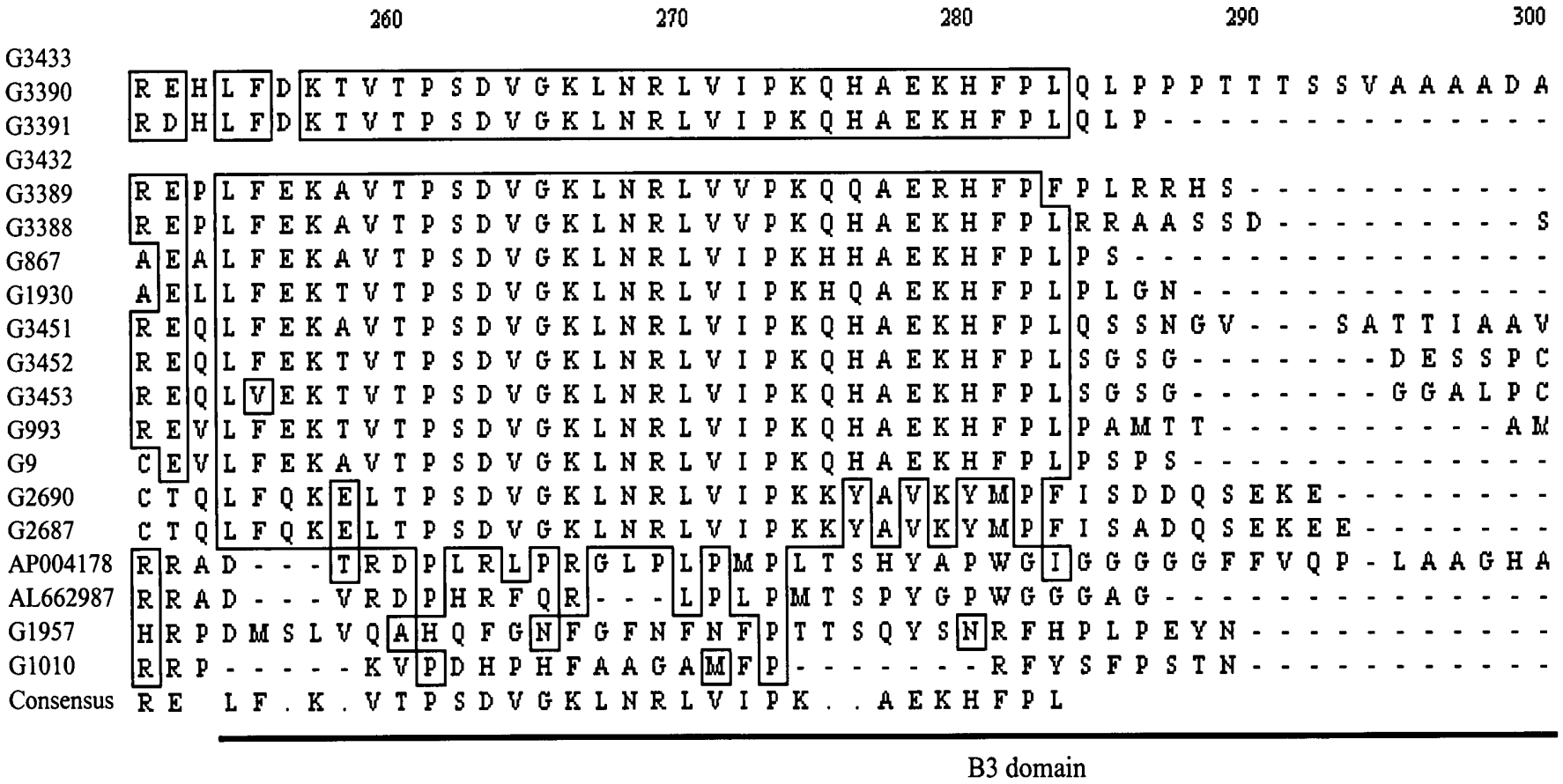

260
270
280
290
300
G3433
G3390 REHLFDKTVTPSDVGKLNRLVIPKQHAEKHFPLQLPPPTTTSSVAAAADA
G3391 RDHLFDKTVTPSDVGKLNRLVIPKQHAEKHFPLQLP----------
G3432
G3389 REPLFEKAVTPSDVGKLNRLVVPKQQAERHFPFPLRRHS----------
G3388 REPLFEKAVTPSDVGKLNRLVVPKQHAEKHFPLRRAASSD---------S
G867 AEALFEKAVTPSDVGKLNRLVIPKHHAEKHFPLPS----------
G1930 AELLFEKTVTPSDVGKLNRLVIPKHQAEKHFPLPLGN----------
G3451 REQLFEKAVTPSDVGKLNRLVIPKQHAEKHFPLQSSNGV---SATTIAAV
G3452 REQLFEKTVTPSDVGKLNRLVIPKQHAEKHFPLSGSG-------DESSPC
G3453 REQLVEKTVTPSDVGKLNRLVIPKQHAEKHFPLSGSG-------GGALPC
G993 REVLFEKTVTPSDVGKLNRLVIPKQHAEKHFPLPAMTT----------AM
G9 CEVLFEKAVTPSDVGKLNRLVIPKQHAEKHFPLPSPS----------
G2690 CTQLFQKELTPSDVGKLNRLVIPKKYAVKYMPFISDDQSEKE---------
G2687 CTQLFQKELTPSDVGKLNRLVIPKKYAVKYMPFISADQSEKEE---------
AP004178 RRAD---TRDPLRLPRGLPLPMPLTSHYAPWGIGGGGGFFVQP-LAAGHA
AL662987 RRAD---VRDPHRFQR---LPLPMTSPYGPWGGGAG----------
G1957 HRPDMSLVQAHQFGNFGFNFNFPTTSQYSNRFHPLPEYN----------
G1010 RRP-----KVPDHPHFAAGAMFP-------RFYSFPSTN----------
Consensus RE LF.K.VTPSDVGKLNRLVIPK..AEKHFPL
B3 domain

FIGURE 4F

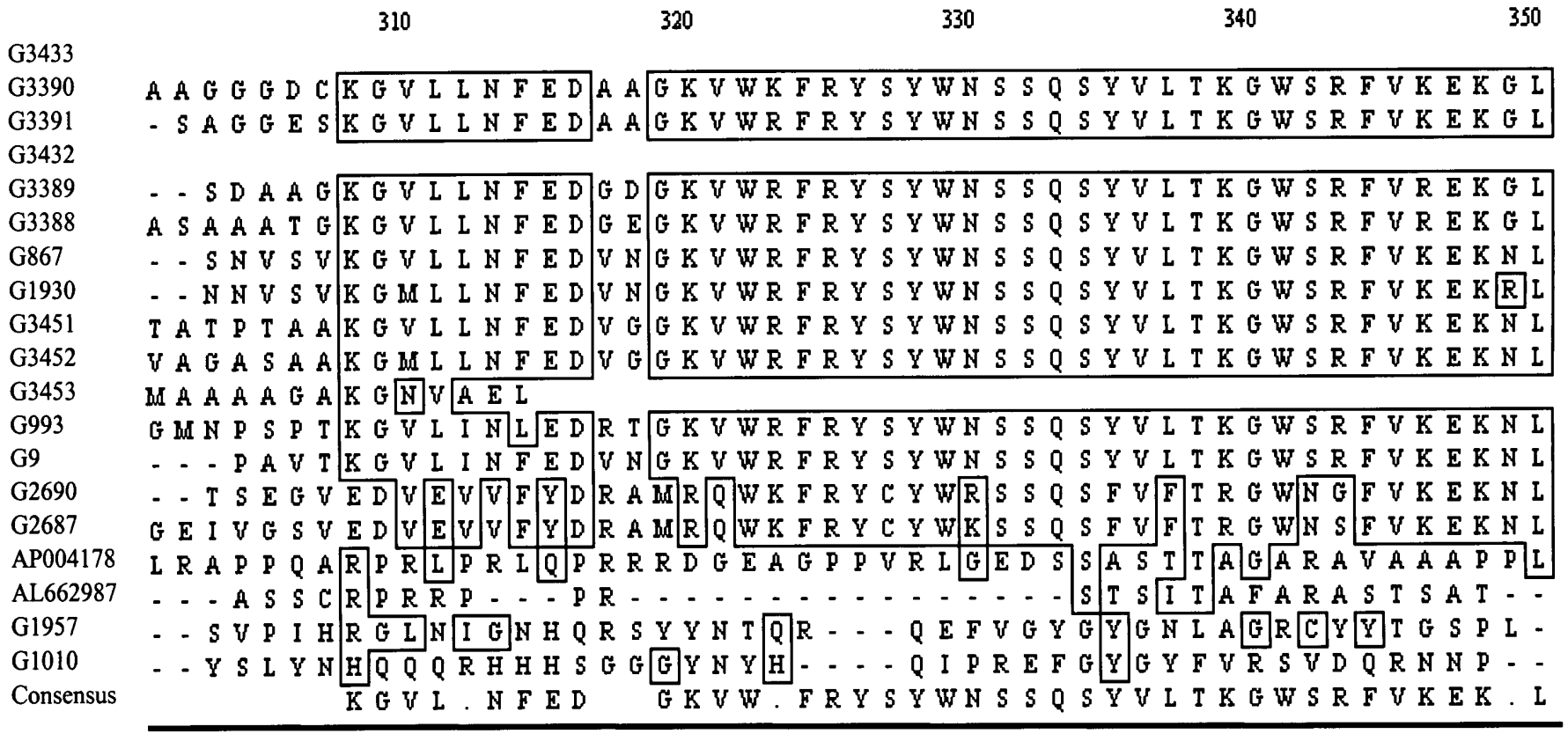

310
320
330
340
350
G3433
G3390 AAGGGDCKGVLLNFEDAAGKVWKFRYSYWNSSQSYVLTKGWSRFVKEKGL
G3391 -SAGGESKGVLLNFEDAAGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKGL
G3432
G3389 --SDAAGKGVLLNFEDGDGKVWRFRYSYWNSSQSYVLTKGWSRFVREKGL
G3388 ASAAATGKGVLLNFEDGEGKVWRFRYSYWNSSQSYVLTKGWSRFVREKGL
G867 --SNVSVKGVLLNFEDVNGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNL
G1930 --NNVSVKGMLLNFEDVNGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKRL
G3451 TATPTAAKGVLLNFEDVGGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNL
G3452 VAGASAAKGMLLNFEDVGGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNL
G3453 MAAAAGAKGNVAEL
G993 GMNPSPTKGVLINLEDRTGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNL
G9 ---PAVTKGVLINFEDVNGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNL
G2690 --TSEGVEDVEVVFYDRAMRQWKFRYCYWRSSQSFVFTRGWNGFVKEKNL
G2687 GEIVGSVEDVEVVFYDRAMRQWKFRYCYWKSSQSFVFTRGWNSFVKEKNL
AP004178 LRAPPQARPRLPRLQPRRRDGEAGPPVRLGEDSSASTTAGARAVAAAPPL
AL662987 ---ASSCRPRRRP---PR----------STSITAFARASTSAT--
G1957 --SVPIHRGLNIGNHQRSYYNTQR---QEFVGYGYGNLAGRCYYTGSPL-
G1010 --YSLYNHQQQRHHHSGGGYNYH----QIPREFGYGYFVRSVDQRNNP--
Consensus KGVL.NFED GKVW.FRYSYWNSSQSYVLTKGWSRFVKEK.L
B3 domain

FIGURE 4G

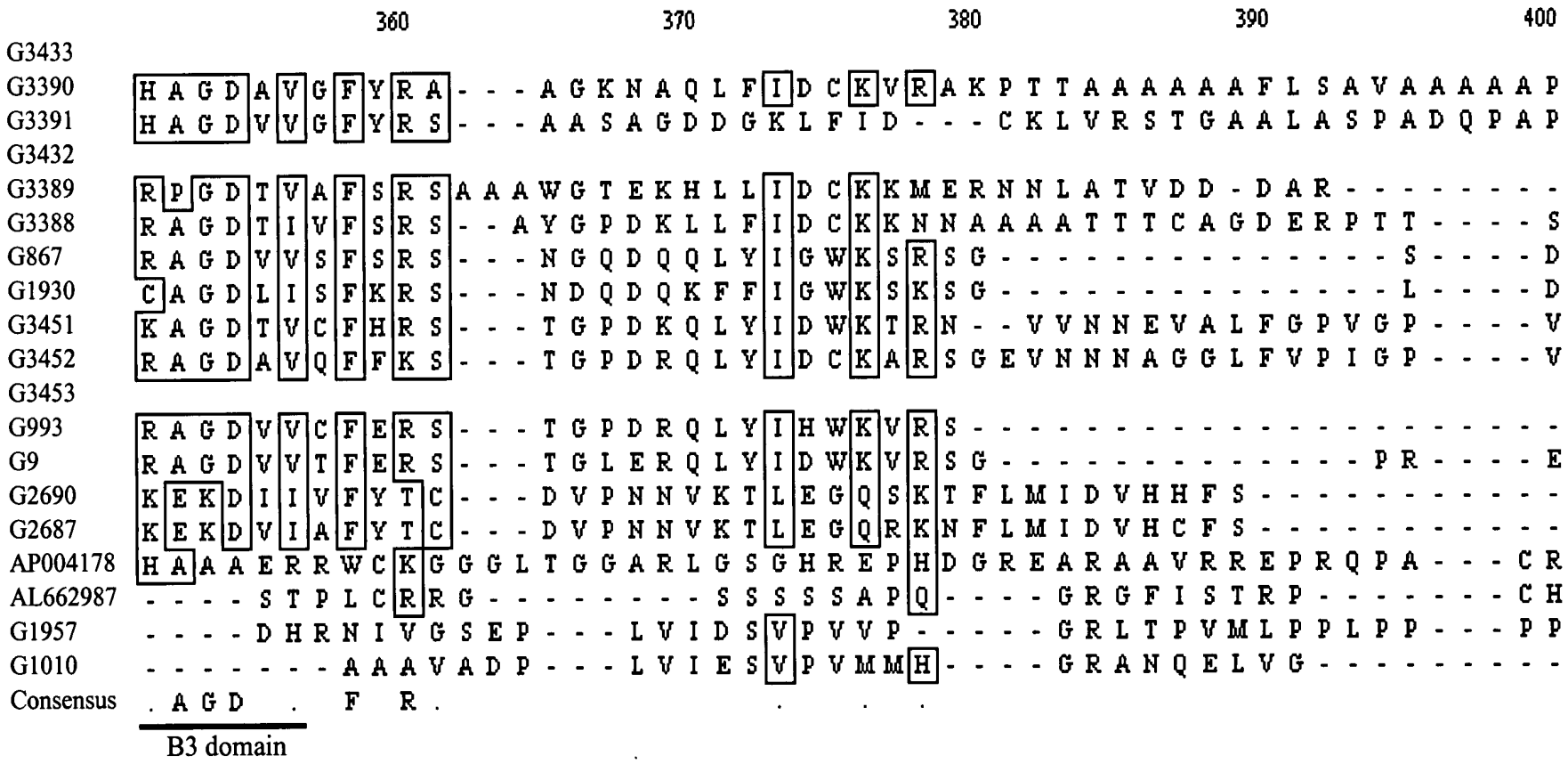
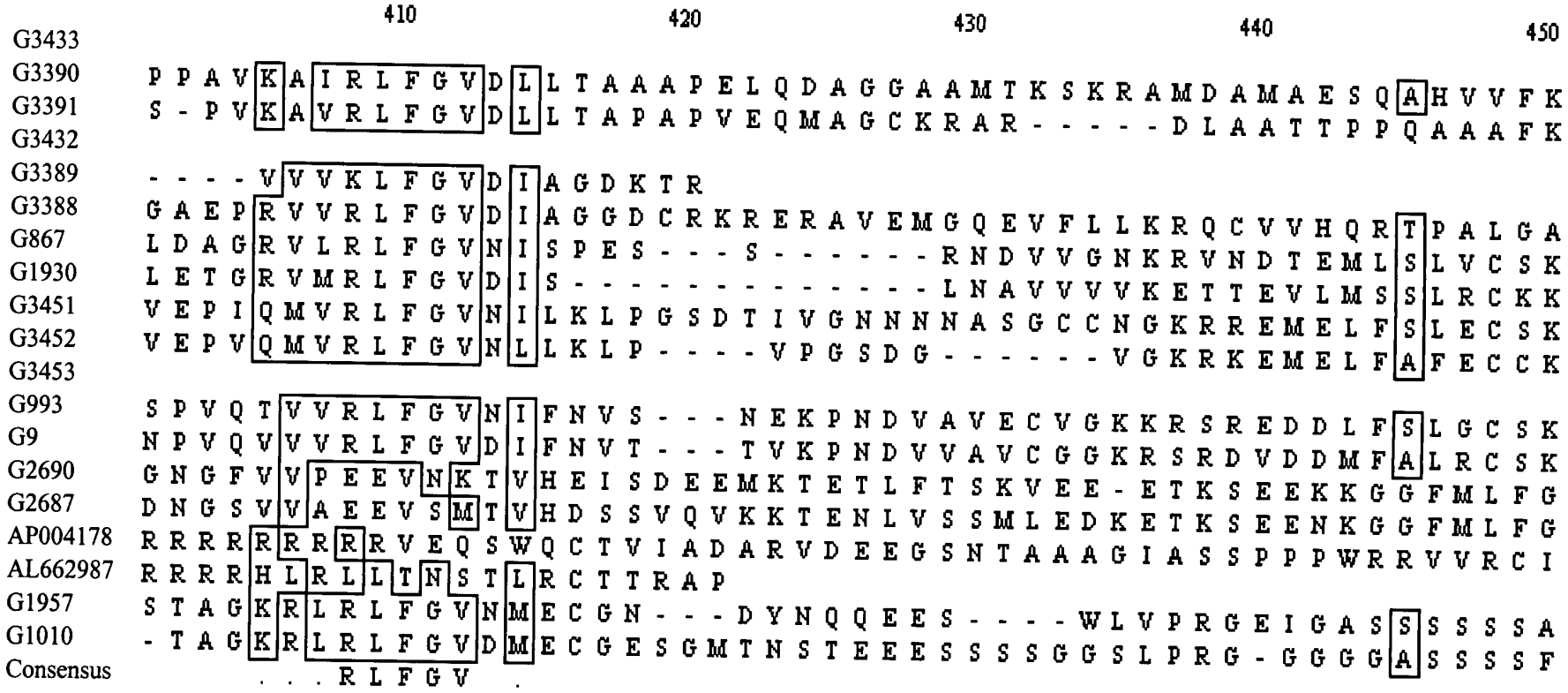

360
370
380
390
400
G3433
G3390 HAGDAVGFYRA---AGKNAQLFIDCKVRAKPTTAAAAAAAFLSAVAAAAAP
G3391 HAGDVVGFYRS---AASAGDDGKLFID---CKLVRSTGAALASPADQPAP
G3432
G3389 RPGDTVAFSRSAAAWGTEKHLLIDCKKMERNNLATVDD-DAR---------
G3388 RAGDTIVFSRS--AYGPDKLLFIDCKKNNAAAATTTCAGDERPTT----S
G867 RAGDVVSFSRS---NGQDQQLYIGWKSRSG----------------S----D
G1930 CAGDLISFKRS---NDQDQKFFIGWKSKSG----------------L----D
G3451 KAGDTVCFHRS---TGPDKQLYIDWKTRN--VVNNEVALFGPVGP----V
G3452 RAGDAVQFFKS---TGPDRQLYIDCKARSGEVNNNAGGLFVPIGP----V
G3453
G993 RAGDVVCFERS---TGPDRQLYIHWKVRS----------------------
G9 RAGDVVTFERS---TGLERQLYIDWKVRSG----------------PR----E
G2690 KEKDIIVFYTC---DVPNNVKTLEGQSKTFLMIDVHHFS----------
G2687 KEKDVIAFYTC---DVPNNVKTLEGQRKNFLMIDVHCFS----------
AP004178 HAAAERRWCKGGGLTGGARLGSGHREPHDGREARAAVRREPRQPA---CR
AL662987 -----STPLCRRG----------SSSSSAPQ----GRGFISTRP-------CH
G1957 ----DHRNIVGSEP---LVIDSVPVVP-----GRLTPVMLPPLPP---PP
G1010 -------AAAVADP---LVIESVPVMMH----GRANQELVG---------
Consensus .AGD.F R.
B3 domain

FIGURE 4H


410
420
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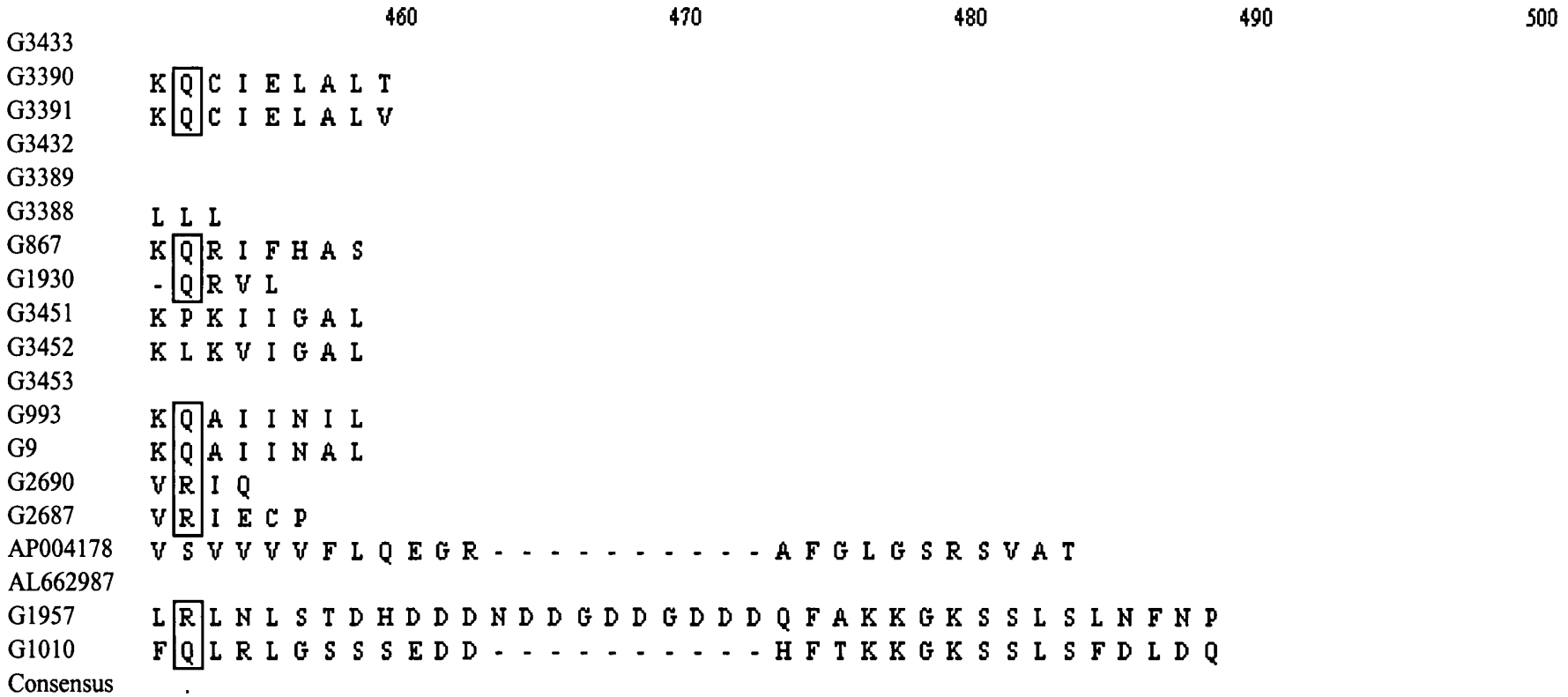
450
G3433
G3390 P P A V K A I R L F G V D L L T A A A P E L Q D A G G A A M T K S K R A M D A M A E S Q A H V V F K
G3391 S - P V K A V R L F G V D L L T A P A P V E Q M A G C K R A R - - - - - D L A A T T P P Q A A A F K
G3432
G3389 - - - - V V V K L F G V D I A G D K T R
G3388 G A E P R V V R L F G V D I A G G D C R K R E R A V E M G Q E V F L L K R Q C V V H Q R T P A L G A
G867 L D A G R V L R L F G V N I S P E S - - - S - - - - - - - R N D V V G N K R V N D T E M L S L V C S K
G1930 L E T G R V M R L F G V D I S - - - - - - - - - - - - - - - L N A V V V V K E T T E V L M S S L R C K K
G3451 V E P I Q M V R L F G V N I L K L P G S D T I V G N N N N A S G C C N G K R R E M E L F S L E C S K
G3452 V E P V Q M V R L F G V N L L K L P - - - - V P G S D G - - - - - - V G K R K E M E L F A F E C C K
G3453
G993 S P V Q T V V R L F G V N I F N V S - - - N E K P N D V A V E C V G K K R S R E D D L F S L G C S K
G9 N P V Q V V V R L F G V D I F N V T - - - T V K P N D V V A V C G G K R S R D V D D M F A L R C S K
G2690 G N G F V V P E E V N K T V H E I S D E E M K T E T L F T S K V E E - E T K S E E K K G G F M L F G
G2687 D N G S V V A E E V S M T V H D S S V Q V K K T E N L V S S M L E D K E T K S E E N K G G F M L F G
AP004178 R R R R R R R R R V E Q S W Q C T V I A D A R V D E E G S N T A A A G I A S S P P P W R R V V R C I
AL662987 R R R R H L R L L T N S T L R C T T R A P
G1957 S T A G K R L R L F G V N M E C G N - - - D Y N Q Q E E S - - - - W L V P R G E I G A S S S S S S A
G1010 - T A G K R L R L F G V D M E C G E S G M T N S T E E E S S S S G G S L P R G - G G G G A S S S S F
Consensus . . . R L F G V .

FIGURE 4I


460
470
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490
500
G3433
G3390 K Q C I E L A L T
G3391 K Q C I E L A L V
G3432
G3389
G3388 L L L
G867 K Q R I F H A S
G1930 - Q R V L
G3451 K P K I I G A L
G3452 K L K V I G A L
G3453
G993 K Q A I I N I L
G9 K Q A I I N A L
G2690 V R I Q
G2687 V R I E C P
AP004178 V S V V V V F L Q E G R - - - - - - - - - - A F G L G S R S V A T
AL662987
G1957 L R L N L S T D H D D D N D D G D D G D D D Q F A K K G K S S L S L N F N P
G1010 F Q L R L G S S S E D D - - - - - - - - - - H F T K K G K S S L S F D L D Q
Consensus

FIGURE 4J

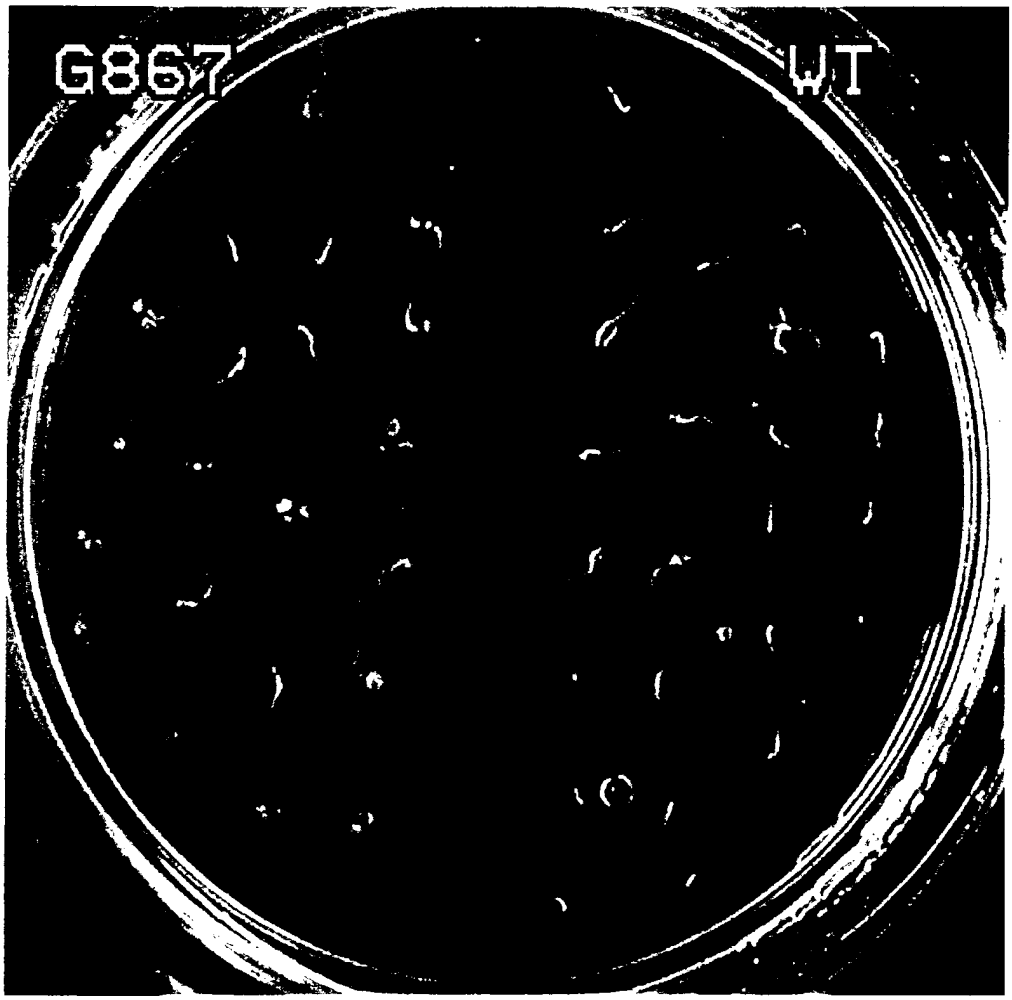

FIGURE 5

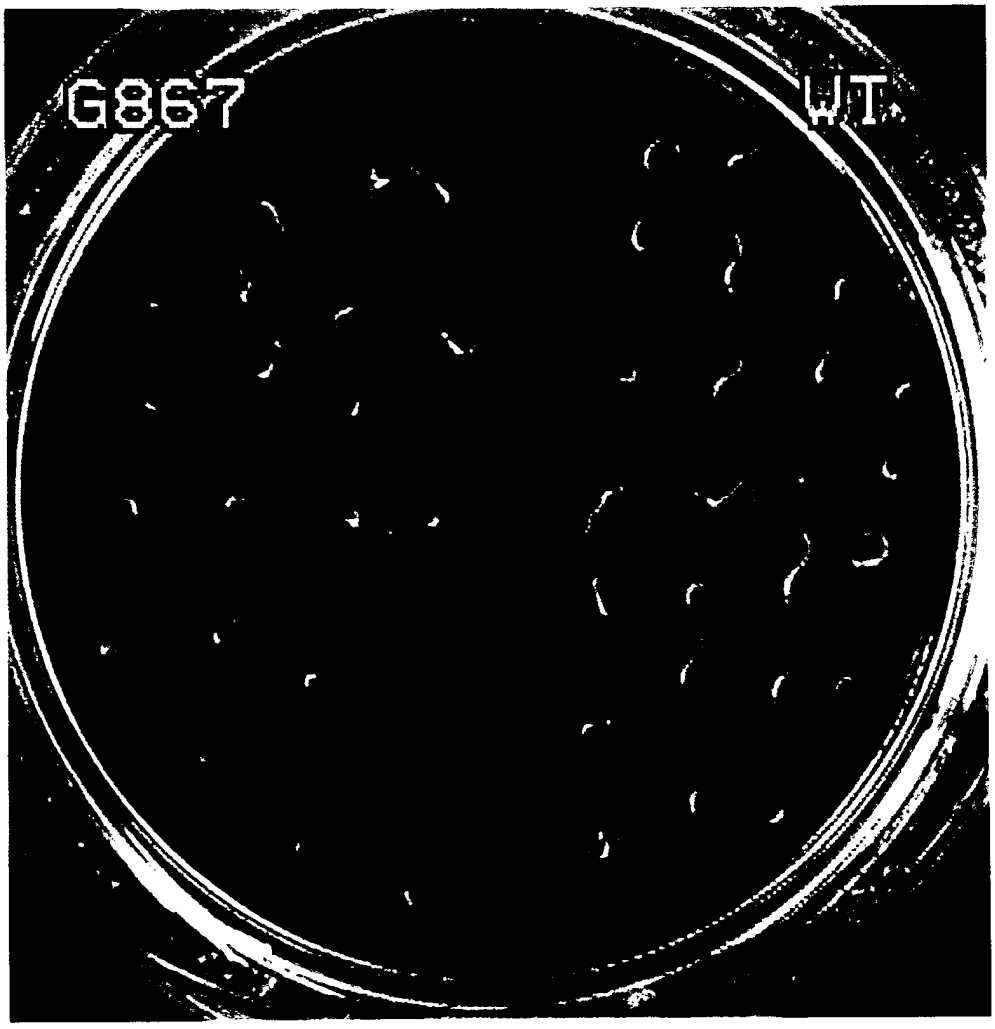

FIGURE 6

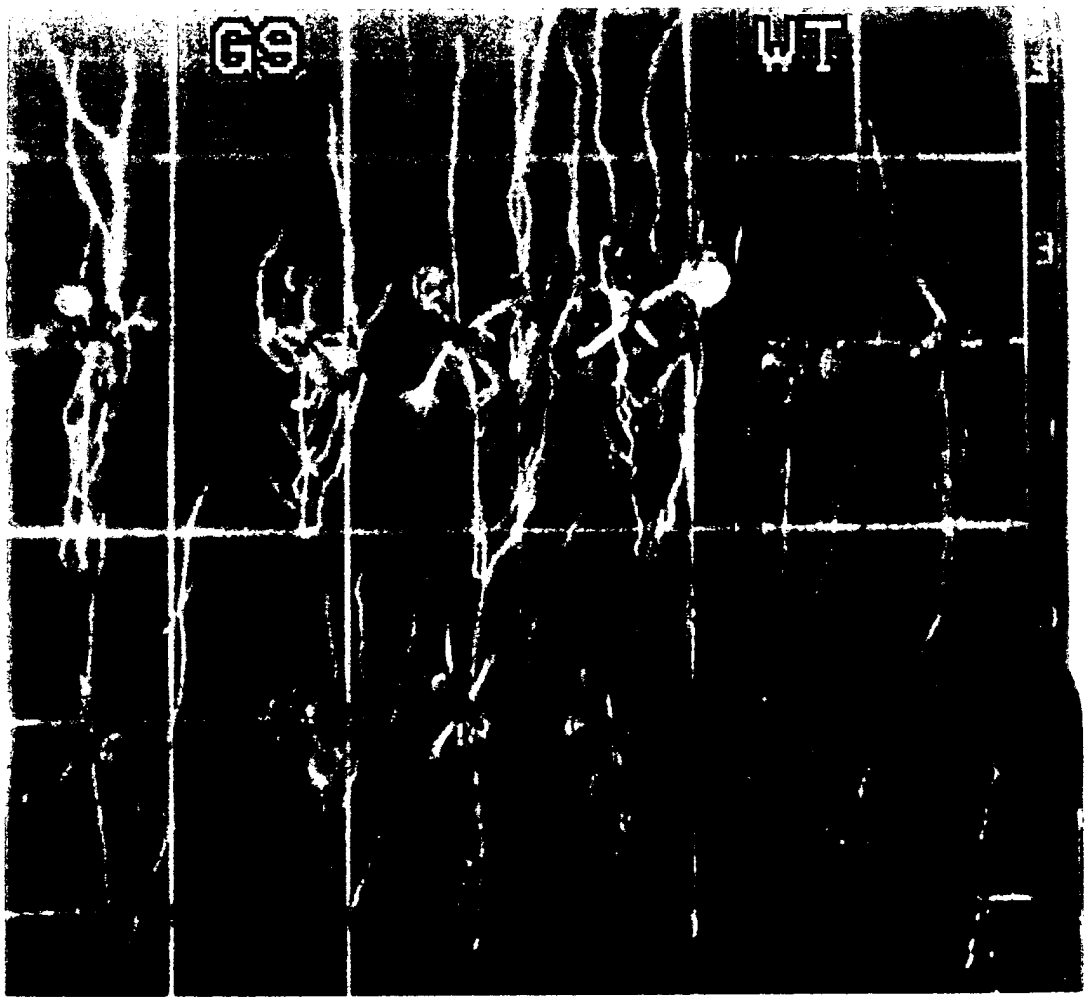

FIGURE 7

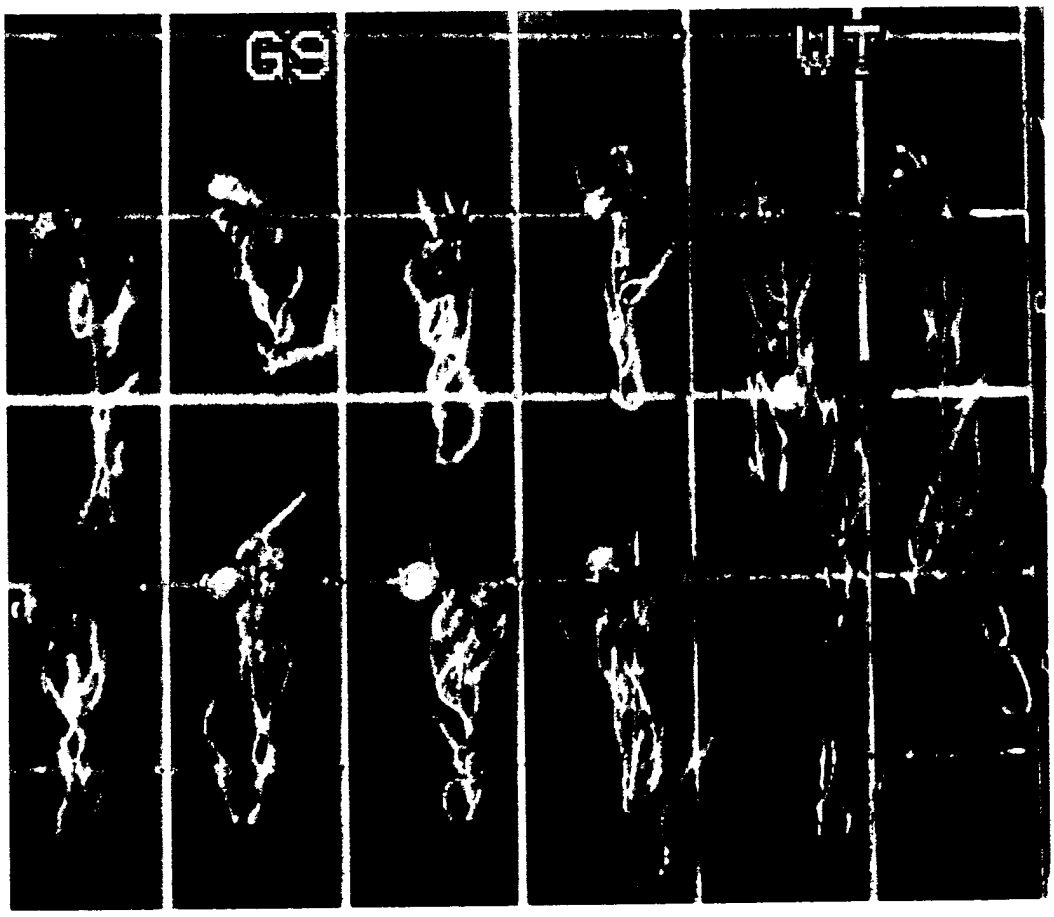

FIGURE 8